P26 13 MONTE CARLO SIMULATIONS OF CHROMOSOME ABERRATIONS COMPARED TO CYTOGENETIC DATA.

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A Monte Carlo program was developed based on the breakage-and-reunion model for radiation-induced chromosome aberrations. Proximity effects due to localization of chromosome interactions in space and time were included. Two adjustable parameters were used. One corresponds to the total radiation dose and the other determines proximity effects by specifying the number of "interaction sites" in the cell nucleus. The data modeled included recent FISH results for 3-color chromosome painting and for 2-color painting with a pan-centromere probe. For any FISH scoring, the analysis allows systematic extrapolation from observed damage to whole-genome damage, taking the actual arm-lengths of all chromosomes into account. Extrapolation showed that complex rearrangements are common for a 1.89 Gy gamma-ray dose. Data simulated also included (a) extensive data on the statistical distribution of dicentrics per cell; (b) ratios of dicentrics to centric rings; and (c) G-banding data from A-bomb survivors. With about 5 to 15 interaction sites in the human cell nucleus, agreement between the experiments and the simulations was within a factor of 2 or better, even when quite detailed categories of damage were scored. Monte Carlo methods adequately accounted for proximity effects, and gave good quantitative estimates, with a minimum of adjustable parameters or theoretical assumptions.